



(SEQ ID:3) 1 AGCTCACAGCC 11
12 ATGGTTACCTTCAGCCACGTCTCCAAGTCTGAGTCACTGGTTCCCTCTTGCTGCTGCTGCTG 71
(SEQ ID:1) 1 M V T F S H V S S L S H W F L L L L L L 20
72 AATCTGTTCTTGCCGGTAATATTTGCTATGCCTGAATCATACTCCTTCAACTGTCCCGAT 131
21 N L F L P V I F A M P E S Y S F N C P U 40
132 GGTGAATACCAGTCTAATGATGTCTGTTGCAAGACCTGTCCCTCAGGTACATTTGTCAAG 191
41 G E Y Q S N D V C C K T C P S G T F V K 60
192 GCGCCCTGCAAAATCCCCATACTCAAGGACAATGTGAGAAGTGTACCCAGGAACATTC 251
61 A P C K I P H T Q G Q C E K C H P G T F 80
252 ACAGGGAAGATAATGGCCTGCATGATTGTGAACCTTTGCTCCACCTGTGATAAAGACCAG 311
81 T G K D N G L H D C E L C S T C D K D Q 100
312 AATATGGTGGCTGACTGTTCTGCCACCAAGTGACCGGAAATGCGAGTGCCAAATAGGTCTT 371
101 N M V A D C S A T S D R K C E C Q I G L 120
372 TACTACTATGACCCAAAATTTCCGGAATCATGCCGCCATGTACCAAGTGTCCCAAGGA 431
121 Y Y Y D P K F P E S C R P C T K C P Q G 140
432 ATCCCTGTCTCCAGGAATGCAACTCCACAGCTAACACTGTGTGCAGTTCATCTGTTTCA 491
141 I P V L Q E C N S T A N T V C S S S V S 160
492 AATCCCAGAACTGGCTGTTCTACTGATGCTAATTGTCTTCTGTATCTGA 542
161 N P R N W L F L L M L I V F C I * 177
543 AGAAGATAAAGGTTCTACAGATGGTGTCTGTAGCTTCCTTTTATTGCTGTGAAGAGAA 600
601 ACCATGGAGGCAACTCTTTTCATTTTATTTTATTTTAAATGTCTTGAACCTTGATTTGAAG 660
661 ACCAGGCTGGACTCAAACCTCACAGAGATCCGGACTAGGCACCTCTAATATAGGAAAACAT 720
721 TGAATTGGGACTGGCTTACAGTTTCAGAAGTTCTGTCCATGATTATCATAGTGCGAAGCA 780
781 TGGAGGCACGGAGGCACACATGGTGTGGAGAAGAAGCTGAGAGTTCTGCATCTTGATCT 840
841 GCAAGCAATAAAAGGAGACTGTGTGCCACACTACACATAGCTTGAACATAGGAGACCTCA 900
901 AAGCCTGTCCCCACAGTGACAACTTCCTCCAACAAGGTCATACCTCCTAATAATACCAT 960
961 TTCTTATGAGGCAAGCATTCAAACACATGAGTCTATGAGGGCCAAACCAATTCAAACCAC 1020
1021 CACAGGTTAACAATTGCCCTCTGCAGCTCTCTGGTGGAGGCCCTCCTTGAGAGTAAGTAA 1080
1081 CAATTTAGATGAAGGCAAGTCTGATCAGGTCCAAAAGAACTCAGGATGAATGGTCC 1140
1141 ACTGTGGTTCTATTAACTACTGAAGAACATGACCTCACCTTAGACTTCTCCACCTCAC 1200
1201 TGGCTTCCCTTCCCTAGCTTCTCATTTCCAGGTAACCCTGCCATTTTTTGGTAATGTGC 1260
1261 CTTCTTGGTTCTTCTCTCCTTTCCCTCTCTTCTGCTCTTATTTCTCTTCTCTCCC 1320
1321 ACTCTCCACCAGCCGCTCTTAAGGCCTGAGTCAGTCTGCAGGCCATGTTTAATCTACTA 1380
1381 CTTTCTCTGTCTGTGACTCATCCAGATGTCTCTGGCTGAGCTCTCCCTCCTATCTACA 1440
1441 ATAAAACCTTCCCCCTAACCAGAAATGGAACAGTTTGTCTCACTTTGTACATCTGGTG 1500
1501 CCTGAAACC 1509

FIG. 1

(SEQ ID:14) 7F4 CPDGEY---QSNDVC CKTCPSGTFVKAPCK IPHTQQCEKCHPGT FTGKDNGLHDCETCS 60

(SEQ ID:13) mTNFR CPGGKYVHSKNNSIC GTKCHKGTYLVSDCP SPGRDTVGRECEKGT FTASQNYLRQCLSK 60

7F4 ICDKD--QNMVADCS ATSDRKCEC---QIG LYYDPKFPESCRPC TKCPQGIPVLQECNS 120

mTNFR ICRKEMSQVEISPCQ ADKDTVCGCKENQFQ RYLSETHFQ--CVDC SPCFNGTVTIP-CKE 120

7F4 TANTVC

126

mTNFR IQNTVC

126

FIG. 2